

META-ANALYSIS OF GENETIC PARAMETERS FOR ECONOMIC TRAITS IN RABBIT USING A RANDOM-EFFECTS MODEL

Nandrya Hayne Santos Lima¹*, Elizangela Zayana Lima D'suze¹*, Denise de Assis Paiva¹†, Nilsa Duarte da Silva Lima¹*, Thalles Ribeiro Gomes¹*, José Teodoro de Paiva¹*

*Department of Animal Science, Federal University of Roraima, BOA VISTA, Roraima, Brazil.

†Department of Statistics, Federal University of Lavras, LAVRAS, Minas Gerais, Brazil.

Abstract: The genetic improvement of rabbits helps increase their productivity and, consequently, increase the supply of animal protein for human consumption. The aim of this study was to perform a meta-analysis of genetic parameters (heritability and genetic correlation) for litter size at birth, litter weight at birth, litter size at weaning, litter weight at weaning and slaughter weight in rabbits. The final dataset contained 147 estimates of heritability and 32 estimates of genetic correlation across 34 articles published between 1992 and 2022. A random-effects model was used and the heterogeneity of estimates was assessed using Q and I^2 statistics. Heritability estimates were of low magnitude for all traits, ranging from 0.09 to 0.18. The lowest heritability estimate was observed for litter size at weaning and the highest for slaughter weight. Most genetic correlations between traits were positive and moderate, ranging from 0.44 to 0.60. Significant heterogeneity among studies justified the use of random-effects models. The meta-analysis study provided reliable genetic parameter estimates and these results can support the development of rabbit breeding programmes.

Key Words: genetic correlation, heritability, heterogeneity, genetic selection, rabbit.

INTRODUCTION

Rabbit (*Oryctolagus cuniculus*) production has evolved over the years due to its potential for meat, fur, laboratory animal, pharmaceutical industry, biological production and other purposes of commercial interest (Dige *et al.*, 2012). In 2019, global rabbit meat production reached 883 936 tonnes, becoming a source of quality animal protein in developing countries (Kumar *et al.*, 2023). These animals have high fecundity and prolificacy, being an economic alternative in urban and rural areas (Montes-Vergara *et al.*, 2021). Genetic improvement of rabbits contributes to increased herd productivity and supply of animal protein for human consumption. When selecting these animals, it is essential to know the genetic parameters of traits of economic importance in the production system. Traits such as litter size, litter weight and body weight are some of the aspects that have been evaluated in rabbit breeding programmes (Sakthivel *et al.*, 2017; Farouk *et al.*, 2022). Among these traits, litter size at birth has the greatest economic value (Nguyen *et al.*, 2017) in prolific species. The number of young rabbits achieved in commercial lines depends on the number kits born alive and their postnatal survival. Rabbits with larger birth weight have higher body weight at their first mating, as well as during their reproductive life (Szendrő *et al.*, 2019). The decision on selection criteria should consider the knowledge of the genetic architecture that these traits present in the population and how they are associated.

Correspondence: J.T. Paiva, jose.paiva@ufr.br. Received December 2023 - June 2024.
<https://doi.org/10.4995/wrs.2024.20933>

Cite as: Lima N.H.S., D'suze E.Z.L., Paiva D.A., Lima N.D.S., Gomes T.R., Paiva J.T. 2024. Meta-analysis of genetic parameters for economic traits in rabbit using a random-effects model. *World Rabbit Sci.*, 32: 175-191. <https://doi.org/10.4995/wrs.2024.20933>

In this sense, meta-analysis employs statistical methods to combine and summarise the results from multiple independent scientific studies (Sutton *et al.*, 2000). In the context of rabbit breeding, meta-analysis affords synthesised knowledge of the genetic parameters for economically important traits. In animal breeding programmes, the application of meta-analysis study helps obtain useful estimates of the parameters that could support genetic evaluations when reliable estimates for traits in rabbit are not available (Oliveira *et al.*, 2017). Previous studies have provided genetic parameter estimates for several crucial economic traits in rabbits, including litter size at birth, litter weight at birth, litter size at weaning and litter weight at weaning (Sakthivel *et al.*, 2017; Ezzeroug *et al.*, 2019; Farouk *et al.*, 2022). However, these estimates are derived from populations with different sample sizes, breed and statistical models. In addition, there is a high variability in the estimates obtained in different studies, mainly due to genetic differences within and between breeds (Akanno *et al.*, 2013). Therefore, a meta-analysis considering the variability between studies appears as a practical and efficient solution (Sutton *et al.*, 2000).

Meta-analysis based on random-effects models is a statistical tool used to provide estimates closer to the true unknown parameters (Oliveira *et al.*, 2017). According to Borenstein *et al.* (2009), the results of meta-analysis using random-effects models can be considered more reliable than those obtained from individual studies and may be applied to a large reference population. However, meta-analysis for genetic parameters of economic traits in rabbits has not yet been reported in the literature, being a field of research to be explored in the genetic improvement of rabbits.

The aim of this study was to perform a meta-analysis of genetic parameters (heritability and genetic correlation) for traits of economic importance in rabbits using random-effects models.

MATERIALS AND METHODS

Literature search and Traits

Initially, a literature review was performed to identify all references that reported estimates of genetic parameters (heritability and genetic correlation) for economic traits in rabbit populations. The traits analysed were: litter size at birth (LSB), litter weight at birth (LWB), litter size at weaning (LSW), litter weight at weaning (LWW) and slaughter weight (SW). The following search strategies and selection criteria were considered for the review of this study: (1) search for articles published from 1992 to 2022 on access platforms: Web of Science, PubMed, Google Scholar and Scopus; (2) search terms applied to extract potentially relevant articles, such as “genetic parameters”, “heritability”, “genetic correlation”, “rabbits”, “growth traits”, “litter size at birth”, “litter weight at birth”, “litter size at weaning”, “litter weight at weaning” and “slaughter weight”. Alternative or combined words were also allowed and (3) only scientific articles published with informative descriptions for the estimates were considered. Studies of all formats and languages were admitted according to the search terms mentioned above.

Data recording and exploratory analysis

A database was constructed containing genetic parameters information for all traits evaluated. In addition, the following were recorded: year of publication, journal name, number of phenotypic records, phenotypic mean, standard deviation, coefficient of variation and model statistical details. Genetic parameter estimates were derived from different methods: Henderson’s method, restricted maximum likelihood method or Bayesian inference in a mixed animal model. For some published genetic parameter estimates, the standard error (SE) was not reported, and in these cases the approximate standard error was calculated using the pooled variance method, as described by Sutton *et al.* (2000):

$$SE_{ij} = \sqrt{\left(\frac{\sum_{k=1}^k s_{ik}^2 n_{ik}^2 / \sum_{k=1}^k n_{ik}}{n_{ij}} \right)} \quad (1)$$

where SE_{ij} is the predicted SE for the published parameter estimate for the j^{th} trait in the j^{th} study that has not reported the SE, s_{ik} is the published SE for the parameter estimate for the i^{th} trait in the k^{th} study that has reported the SE,

n_k is the number of records used to predict the published parameter estimate for the i^{th} trait in the k^{th} study that has reported the SE, and n_j' is the number of used records to predict the published parameter estimate for the i^{th} trait in the j^{th} study that has not reported the SE.

Most meta-analysis studies in animal breeding do not use the published genetic correlation estimates because they do not follow a normal distribution (Oliveira *et al.*, 2017). Thus, the genetic correlation estimates published were first transformed to an approximate normal scale by using the Fisher's Z transformation, as described below (Borenstein *et al.* 2009):

$$Z_{ij,k} = 0.5[\ln(1 + r_{g_{ij,k}}) - \ln(1 - r_{g_{ij,k}})] \quad (2)$$

where $Z_{ij,k}$ and $r_{g_{ij,k}}$ are, respectively, the transformed and published genetic correlation estimates among traits i and j in the k^{th} study.

As noted by Hossein-Zahed (2021), the results of the meta-analysis, such as the estimated parameter and its confidence interval, would then be converted back to correlations for presentation using the following equation:

$$r_{g_{ij,k}}^* = (e^{2Z_{ij,k}} - 1) / (e^{2Z_{ij,k}} + 1) \quad (3)$$

where $r_{g_{ij,k}}^*$ is the re-transformed genetic correlation estimate and $Z_{ij,k}^*$ is the output from the meta-analysis random-effects model.

Data quality control

A box plot weighted by the number of records was used to identify possible outliers, which were constructed for each trait assessed. To ensure the reliability of the meta-analysis and avoid biased estimates, a minimum number of scientific articles was calculated for each trait, based on the relative standard error (RSE) (Zarkovich, 1979). A maximum RSE limit of 25% was assumed, as recommended by Oliveira *et al.* (2017), with the higher RSE indicating a greater impact of uncontrolled variation sources on the estimates.

The RSE calculation is obtained as follows (Zarkovich, 1979):

$$RSE_i = \frac{\left(\frac{S_i}{\sqrt{n_i}}\right)}{\bar{x}_i} \times 100 \quad (4)$$

where RSE_i is the relative standard error, S_i is the standard deviation (SD) estimated from the published parameter estimates for the i^{th} trait, n_i is the number of studies that have reported parameter estimates for the i^{th} trait, and \bar{x}_i is the average of parameter estimates for the i^{th} trait.

The total number of records for each trait was calculated as the sum of the number of records in each study found. Means and standard deviations were calculated for all traits by using the sample sizes as weights. In addition, the coefficient of variation (CV) was calculated for each trait:

$$CV_i(\%) = \frac{S_i}{\bar{X}_i} \times 100 \quad (5)$$

where S_i is the SD for the i^{th} trait, and \bar{X}_i is the trait mean.

Meta-analysis

Weighted parameters mean estimates were obtained by fitting a random-effect model for all traits studied. Estimates were assumed to be independent and normally distributed through the Box-Pierce and Shapiro-Wilk tests, respectively, using R software (R Core Team, 2021).

The meta-analysis was performed considering the following random-effects model for each trait:

$$\theta_j = \bar{\theta} + u_j + e_j \quad (6)$$

where $\hat{\theta}_j$ is the published parameter estimate in the j^{th} study, $\bar{\theta}$ is the weighted population parameter mean, u_j is the among-study component of the deviation from the mean, and e_j is the within-study component due to sampling error in the parameter estimate in the j^{th} study. The u_j and e_j were assumed as $u_j \sim N(0, \tau^2)$ and $e_j \sim N(0, \sigma_e^2)$, respectively, where τ^2 is the variance representing the amount of heterogeneity among studies and σ_e^2 is the within-study variance.

The *metaphor* package (Viechtbauer, 2010) available in R software (R Core Team, 2021) was used to perform the meta-analysis. Forest plots were constructed to indicate the effect size of each study, containing the mean estimates of heritability and genetic correlation with the 95% confidence intervals.

Heterogeneity and publication bias

To quantify the degree of heterogeneity (τ^2) between studies and describe the percentage of total variation that is due to heterogeneity rather than chance, the I^2 index was used (Higgins *et al.*, 2003), described as:

$$I^2 = \frac{Q - df}{Q} \times 100 \quad (7)$$

where Q is the statistic (Cochran, 1954) given by:

$$Q = \sum_{j=1}^J w_j (\hat{\theta}_j - \bar{\theta})^2 \quad (8)$$

where w_j is the parameter estimate weight (assumed as the inverse of published sampling variance for the parameter, $(1/s_j^2)$ in the j^{th} study; $\hat{\theta}_j$ is the parameter estimate published in the j^{th} study and $\bar{\theta}$ is the populational parameter weighted mean estimate, both were defined above in the random-effects model. The df is the degrees of freedom ($J - 1$, where J is the number of used studies) of a Chi-squared distribution assumed for the expected Q value on the assumption that $\tau^2=0$.

Variations between studies were assessed using the Q statistic with a significance level set at 0.05, as it has relatively low power with a small number of studies (Huedo-Medina *et al.*, 2006). The I^2 index was also used to measure the degree of heterogeneity.

In addition, the 95% confidence intervals were considered, and the lower and upper limits will be calculated by:

$$LL_{\bar{\theta}} = \bar{\theta} - 1.96 \times SE_{\bar{\theta}}, \quad (9)$$

$$UL_{\bar{\theta}} = \bar{\theta} + 1.96 \times SE_{\bar{\theta}} \quad (10)$$

where $SE_{\bar{\theta}}$ is the predicted standard error for the estimated parameter $\bar{\theta}$, i.e.:

$$SE_{\bar{\theta}} = \sqrt{1 / \sum_{j=1}^J w_j} \quad (11)$$

where all terms were previously described.

Egger's linear regression asymmetry was used to examine the presence of publication bias and a P -value of 0.05 was set. The trim-and-fill method (Duval and Tweedie, 2000) was applied when bias was detected ($P < 0.05$) to find the number of missing studies. In addition, Funnel plots were used to present the asymmetry. When heterogeneity (Q statistic, $P < 0.05$) was detected for the analysed parameter estimates, testing for publication bias is inappropriate since it may lead to positive missing results (Hossein-Zadeh, 2021).

RESULTS

Descriptive statistics

Weighted descriptive statistics for all traits analysed in this study are shown in Table 1. Outliers were found and excluded from the posterior analysis. After quality control, the final dataset contained 147 estimates of heritability

Table 1: Number of articles (NA), number of phenotypic records (NR), mean, standard deviation (SD) and coefficient of variation (CV%) for each trait evaluated in rabbits.

Traits	Abbreviation	Unit	NA	NR	Mean	SD	CV (%)
Litter size at birth	LSB	-	26	245 780	8.68	1.24	14.27
Litter weight at birth	LWB	g	14	15 995	402.43	197.37	49.04
Litter size at weaning	LSW	-	20	167 978	6.58	1.33	20.27
Litter weight at weaning	LWW	g	23	104 852	2920.53	657.02	22.49
Slaughter weight (individual)	SW	g	4	33 469	2104.35	329.82	15.67

and 32 estimates of genetic correlation from 34 peer-reviewed scientific articles published between 1992 and 2022 (Supplementary File S1). Among all the traits evaluated, LWB was found to be highly variable with a CV of 49.04% (Table 1). The weighted coefficients of variation for LSB and SW traits were generally low, 14.27 and 15.67%, respectively.

Heritability

The number of contributing estimates (N), the weighted heritability estimates (h^2), the relative standard error (RSE) and the heterogeneity of the estimates (based on Q and I^2 statistics) obtained from the random-effects meta-analysis are shown in Table 2.

Heritability estimates were of low magnitude for all traits, ranging from 0.09 to 0.18 (Table 2). The lowest heritability estimate was observed for LSW and the highest for SW. All heritability estimates had low standard errors and were statistically significant ($P < 0.05$). In addition, their 95% confidence intervals were narrow and the RSE values were low (<25%), as shown in Table 2. RSE values for heritability estimates ranged from 12.41% (LSB) to 21.68% (LWW). The test for heterogeneity of weighted heritability estimates performed by the Q statistic (Table 2) showed significant heterogeneities ($P < 0.05$). Overall, the I^2 index showed high values (Table 2) for most traits, LWW (96.37%), LSB (90.36%), SW (78.95%) and LSW (88.56%), indicating substantial heterogeneity among studies, except for LWB (47.70%). This suggests the importance of accounting for this variability in the random-effects model used to estimate weighted means in order to obtain reliable estimates.

Results of heritability estimates for evaluated traits obtained from published papers are shown in the Forest plot available in Supplementary Figures 1-5, respectively, for LSB, LWB, LSW, LWW and SW.

Genetic correlation

The mean estimates of genetic correlation for analysed traits are shown in Table 3. Considering the combinations between the five traits studied, a large number of genetic correlations were not available or are limited in the literature. In addition, a few of genetic correlations had to be eliminated from the analysis because their RSE values were greater than 25% (Table 3).

Table 2: Number of estimates (N), heritability (h^2), standard error (SE), 95% confidence interval (95% CI), significance of the random-effect model (P -value), Q statistic (Q) and their significance (P -value), relative standard error (RSE %), and heterogeneity index (I^2 %) estimated through meta-analysis based on random-effects models for each trait evaluated in rabbits.

Traits ¹	N	h^2	SE	95% CI	P -value	Q	P -value	RSE (%)	I^2 (%)
LSB	49	0.11	0.01	0.10-0.13	0.0001	456.59	0.0001	12.41	90.36
LWB	14	0.11	0.01	0.09-0.14	0.0001	28.04	0.0089	21.35	47.70
LSW	33	0.09	0.01	0.07-0.10	0.0001	264.72	0.0001	11.65	88.56
LWW	41	0.11	0.01	0.07-0.14	0.0001	1641.77	0.0001	21.68	96.37
SW	10	0.18	0.02	0.14-0.23	0.0001	77.09	0.0001	18.33	78.95

¹LSB: litter size at birth; LWB: litter weight at birth (g); LSW: litter size at weaning; LWW: litter weight at weaning (g); SW: slaughter weight (g).

Table 3: Number of estimates (N), genetic correlation (r_g), standard error (SE), 95% confidence interval (95% CI), Q statistic (Q), relative standard error (RSE %), and heterogeneity index (I^2 %) estimated through meta-analysis based on random-effects models for each trait evaluated in rabbits.

Traits	N	r_g	SE	95% CI	P -value	Q	P -value	RSE (%)	I^2 (%)
LSB - LSW	10	0.60	0.13	0.44-0.76	0.0001	1843.53	0.0001	15.70	99.50
LSB - LWW	4	0.23	0.08	0.07-0.40	0.0049	0.67	0.8797	22.97	0.00
LSW - LWW	7	0.56	0.22	0.30-0.82	0.0005	536.61	0.0001	19.64	98.22
LSB - LWB	6	0.49	0.15	0.26-0.73	0.0001	5564.21	0.0001	23.81	99.87
LWB - LWW	5	0.44	0.07	0.32-0.56	0.0001	792.49	0.0001	14.53	99.51

LSB: litter size at birth; LWB: litter weight at birth (g); LSW: litter size at weaning; LWW: litter weight at weaning (g).

All genetic correlations for the studied traits were positive and moderate ($P < 0.01$), except for the low association between LSB and LWW (0.23). LSB showed genetic correlation with LSW of 0.60 and with LWB of 0.49, while the estimate found between LSW and LWW was 0.56. Most estimates of genetic correlations (Table 3) showed high heterogeneity and significance among studies (P -value of Q statistic < 0.01 and $I^2 > 98.22\%$), which justifies the use of a random-effects model. The genetic correlation between LSB and LWW showed no significant heterogeneity (Table 3). Results from the statistical test to evaluate publication bias and the trim-and-fill method to correct funnel plot asymmetry in mean genetic correlation between LSB and LWW are shown in Supplementary File S2. The result of Egger's test did not indicate significant publication bias ($P > 0.05$) for genetic correlation between LSB and LWW.

Results of genetic correlation estimates among evaluated traits obtained from published papers are shown in the Forest plot available in Supplementary Figures 6-10, respectively, between LSB and LSW, LSB and LWW, LSW and LWW, LSB and LWB, and LWB and LWW.

DISCUSSION

The literature presents a great variability in the magnitude of genetic parameter estimates for the traits evaluated, emphasising the need to use a random-effect model in the meta-analysis study. To support rabbit breeding programmes, it is crucial that meta-analysis provides solid and reliable estimates of genetic parameters (Oliveira *et al.*, 2017). Thus, the random-effect model was able to consider the sources of variation between and within studies, derived from different populations, breeds, designs and statistical methodologies. The low RSE values suggest acceptable variation in the genetic parameters (heritability and genetic correlation) across the studies, allowing the estimation of combined effects. In addition, there was high heterogeneity among the published studies, as indicated by the Q and I^2 statistics, reinforcing the importance of adopting the random-effect model.

The high number of studies found indicates that there is greater emphasis on the traits collected at birth and weaning in rabbits, in relation to the other. The broad variation in the traits mean shows that there can be considerable variation in the management conditions under which these populations are reared. Individual weight at slaughter had few studies, despite its economic importance in rabbit meat production, perhaps due to the difficulty of measurement or associated cost.

The low weighted mean of heritability estimates found for all evaluated traits were consistent with the literature (Sakthivel *et al.*, 2017; Farouk *et al.*, 2022). These traits are largely influenced by non-additive genetic and environmental effects, including management practices. Nevertheless, there is a portion of additive genetic variance acting on the expression of all traits, suggesting potential improvement through genetic selection. The rabbit population will respond better to direct selection for slaughter weight. Alternatively, selecting for litter size at birth, size weight at birth and size weight at weaning would show similar results in response to selection.

Litter size is one of the most important traits in rabbit breeding and is associated with the high prolificacy of the species. In addition, the survival rate of litters during the lactation period, recorded through the number of animals and weight at weaning, should be highlighted. Rabbit breeding programmes focused on meat production have been established through specialised lines by genetic selection (Moura *et al.*, 2001). Different maternal lines are often selected for reproductive traits such as number of live births, litter size at weaning and weaning weight (Nagy *et al.*,

2011). The direction of selection in paternal lines is focused on improvements in growth and carcass traits (El-Attrouny and Habashy, 2020). Both lines (maternal and paternal) are at the top of the pyramid in breeding programmes as specialised lines and represent the core populations (Moura *et al.*, 2001). The development and maintenance of these lines is a crucial activity for the success of the programmes. To this end, it is necessary to establish direct or indirect selection strategies for litter size traits at birth or weaning (Ragab and Baselga, 2011).

In this context, it is essential to know the genetic associations between the traits used as selection criteria within the lines. According to meta-analysis results, genetic correlation between litter size at birth is positive and moderate with litter weight at birth (0.49) and litter size at weaning (0.60). Based on these results, it can be suggested that selection for litter size at birth would be effective to improve the other traits, and to a lesser extent on litter weight at weaning (0.23). Similarly, it is suggested that selection for litter weight at weaning should achieve moderate genetic gains in the traits of litter weight at birth (0.44) and litter size at weaning (0.56). Thus, a rabbit breeding programme can use a selection index that combines these traits related to litter size and weight at birth and at weaning to optimise the improvement obtained in prolificacy and reproduction traits, as well as in growth rate (Farouk *et al.*, 2022). According to Moura *et al.* (2001), the development of a multi-purpose line could be an interesting alternative through simultaneous selection for prolificacy and growth performance traits in situations where it is not possible to select and maintain specialised sire and dam lines for a subsequent crossbreeding programme. Further research is needed to investigate the effects of selection for the traits evaluated in this study on other economic traits included in the breeding objective.

CONCLUSION

The meta-analysis study provided reliable estimates of heritability and genetic correlations for economic traits in rabbits. There is genetic variability concerning the expression of traits litter size at birth, litter weight at birth, litter size at weaning, litter weight at weaning and slaughter weight. Therefore, improvement in these traits can be achieved by genetic selection. In addition, all traits are genetically associated, suggesting that indirect selection will be efficient way to increase prolificacy and body weight in rabbit production.

Acknowledgements: The authors acknowledge the support of the Federal University of Roraima (PRÓ-PESQUISA/PRPPG) and appreciate the financial support provided by CNPq (Conselho Nacional de Desenvolvimento Científico e Tecnológico).

Authors contribution: Lima N.H.S.: methodology, software, investigation, resources, writing – original draft and visualization; D'Suze E.Z.L.: methodology, investigation and software; Paiva D.A.: validation, formal analysis and investigation; Lima N.D.S.: investigation, methodology and validation; Gomes T.R.: investigation, methodology and validation; Paiva J.T.: conceptualization, methodology, software, validation, formal analysis, investigation, data curation, writing – original draft, visualization, supervision and project administration.

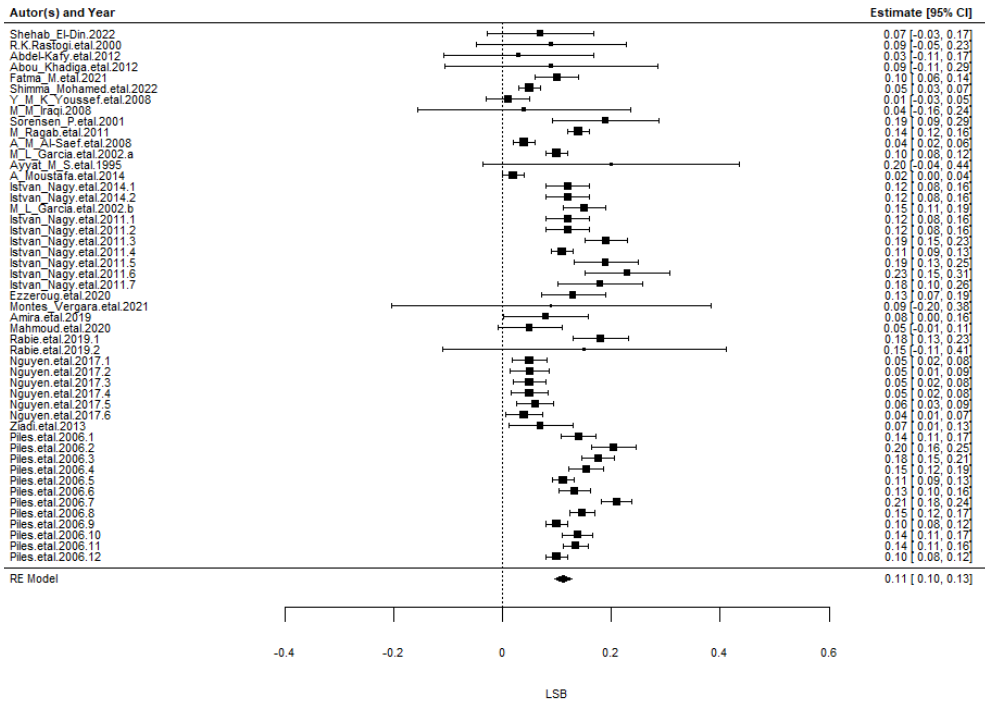
Conflict of interest: The authors declare no conflicts of interest.

REFERENCES

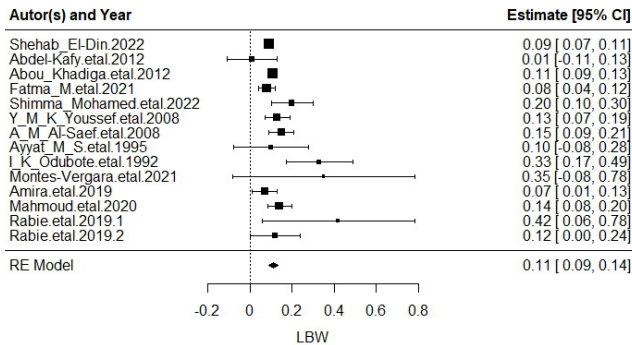
- Akanno E.C., Schenkel F.S., Quinton V.M., Friendship R.M., Robinson J.A.B. 2013. Meta-analysis of genetic parameter estimates for reproduction, growth and carcass traits of pigs in the tropics. *Livest. Sci.*, 152: 101-113. <https://doi.org/10.1016/j.livsci.2012.07.021>
- Borenstein M., Hedges L.V., Higgins J., Rothstein H.R. 2009. Random effects model. In: *Introduction to meta-analysis*, 69-75, Wiley: Chichester, UK. <https://doi.org/10.1002/9780470743386>
- Cochran W.G. 1954. The combination of estimates from different experiments. *Biometrics*, 10: 101-129. <https://doi.org/10.2307/3001666>
- Dige M.S., Kumar A., Kumar P., Dubey P.P., Bhushan B. 2012. Estimation of variance components and genetic parameters for growth traits in New Zealand White rabbit (*Oryctolagus cuniculus*). *J. Appl. Anim. Res.*, 40: 167-172. <https://doi.org/10.1080/09712119.2011.645037>
- Duval S., Tweedie R. 2000. A nonparametric "trim and fill" method of accounting for publication bias in meta-analysis. *J. Am. Stat. Assoc.*, 95: 89-98. <https://doi.org/10.1080/01621459.2000.10473905>
- El-Attrouny M.M., Habashy W.S. 2020. Correlated response on litter traits and milk yield in New Zealand white rabbits selected for litter size at birth. *Egypt Poult Sci.*, 40: 599-612. <https://doi.org/10.21608/EPSJ.2020.114314>

- Ezzeroug R., Belabbas R., Argente M.J., Berbar A., Diss S., Boudjella Z., Talaziza D., Boudahdir N., Garcia M.L. 2019. Genetic correlations for reproductive and growth traits in rabbits. *Can. J. Anim. Sci.*, 100: 317-322. <https://doi.org/10.1139/cjas-2019-0049>
- Farouk S.M., Khattab A.S., Noweir A., Hossein-Zadeh N.G. 2022. Genetic analysis of some productive and reproductive traits in New Zealand White rabbits. *World Rabbit Sci.*, 30: 141-146. <https://doi.org/10.4995/wrs.2022.15939>
- Higgins J.P.T., Thompson S.G., Deeks J.J., Altman D.G. 2003. Measuring inconsistency in meta-analyses. *BMJ*, 327: 557-560. <https://doi.org/10.1136/bmj.327.7414.557>
- Hossein-Zadeh N.G. 2021. A meta-analysis of genetic parameter estimates for conformation traits in horses. *Livest. Sci.*, 250: 104601. <https://doi.org/10.1016/j.livsci.2021.104601>
- Huedo-Medina T.B., Sánchez-Meca J., Marín-Martínez F., Botella J. 2006. Assessing heterogeneity in meta-analysis: Q Statistic Or, I² index? *Psychol. Methods*, 11: 193-206. <https://doi.org/10.1037/1082-989X.11.2.193>
- Kumar S.A., Kim H., Jayasena D.D., Jo C. 2023. On-farm and processing factors affecting rabbit carcass and meat quality attributes. *Food Sci. Anim. Res.*, 43: 197-219. <https://doi.org/10.5851/kosfa.2023.e5>
- Montes-Vergara D.E., Hernández-Herrera D.Y., Hurtado-Lugo N.A. 2021. Genetic parameters of growth traits and carcass weight of New Zealand white rabbits in a tropical dry forest area. *J. Adv. Vet. Anim. Res.*, 8: 471-478. <http://doi.org/10.5455/javar.2021.h536>
- Moura A.S.A.M.T., Costa A.R.C., Polastre R. 2001. Variance components and response to selection for reproductive litter and growth traits through a multi-purpose index. *World Rabbit Sci.*, 9: 77-86. <https://doi.org/10.4995/wrs.2001.449>
- Nagy I., Radnai I., Nagyné-Kiszlinger H., Farkas J., Szendrő Z. 2011. Genetic parameters and genetic trends of reproduction traits in synthetic Pannon rabbits using repeatability and multi-trait animal models. *Arch. Anim. Breed.*, 54: 297-307. <https://doi.org/10.5194/aab-54-297-2011>
- Nguyen N.T., Farkas J., Szendrő Z., Nagy I. 2017. Genetic evaluation of litter size traits in Pannon Large rabbits. *Anim. Sci. Papers and Reports*, 35: 181-192.
- Oliveira H.R., Ventura H.T., Costa E.V., Pereira M.A., Veroneze R., Duarte M.D.S., Siqueira O.H.G.B.D., Silva F.F. 2017. Meta-analysis of genetic parameter estimates for reproduction, growth and carcass traits in Nelore cattle by using a random-effects model. *Anim. Prod. Sci.*, 58: 1575-1061. <https://doi.org/10.1071/AN16712>
- Ragab M., Baselga M. 2011. A comparison of reproductive traits of four maternal lines of rabbits selected for litter size at weaning and founded on different criteria. *Livest. Sci.*, 136: 201-206. <https://doi.org/10.1016/j.livsci.2010.09.009>
- R Core Team. 2021. R: a language and environment for statistical computing. In: *R Foundation for Statistical Computing*, Vienna, Austria.
- Sakthivel M., Balasubramanyam D., Kumarasamy P., Gopi H., Raja A., Anilkumar R., Devaki A. 2017. Estimates of (co)variance components and genetic parameters for body weights and growth efficiency traits in the New Zealand White rabbit. *World Rabbit Sci.*, 25: 329-338. <https://doi.org/10.4995/wrs.2017.7057>
- Sutton A.J., Abrams K.R., Jones D.R., Sheldon T.A., Song F. 2000. In: *Methods for meta-analysis in medical research*. Wiley: Chichester, UK.
- Szendrő Z., Cullere M., Atkári T., Dalle Zotte A. 2019. The birth weight of rabbits: influencing factors and effect on behavioural, productive, and reproductive traits: a review. *Livest. Sci.*, 230: XX. <https://doi.org/10.1016/j.livsci.2019.103841>
- Viechtbauer W. 2010. Conducting meta-analyses in R with the metafor package. *J. Stat. Softw.*, 36: 1-48. <https://doi.org/10.18637/jss.v036.i03>
- Zarkovich S. 1979. Stability of variance patterns. *J Indian Soc Agric Stat.*, 31: 23-48.

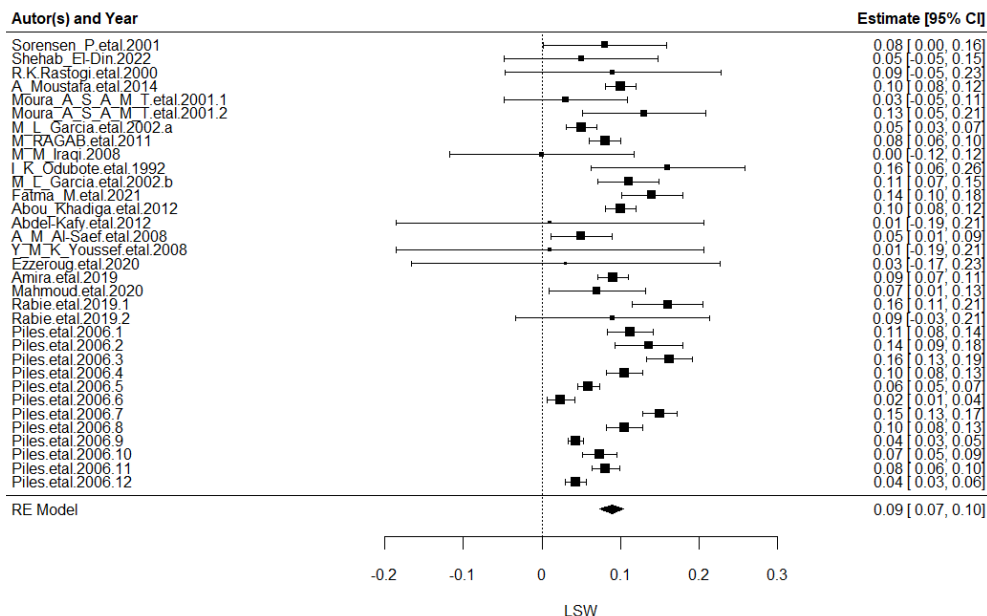
WEIGHTED HERITABILITY AND GENETIC CORRELATION ESTIMATE IN RABBIT



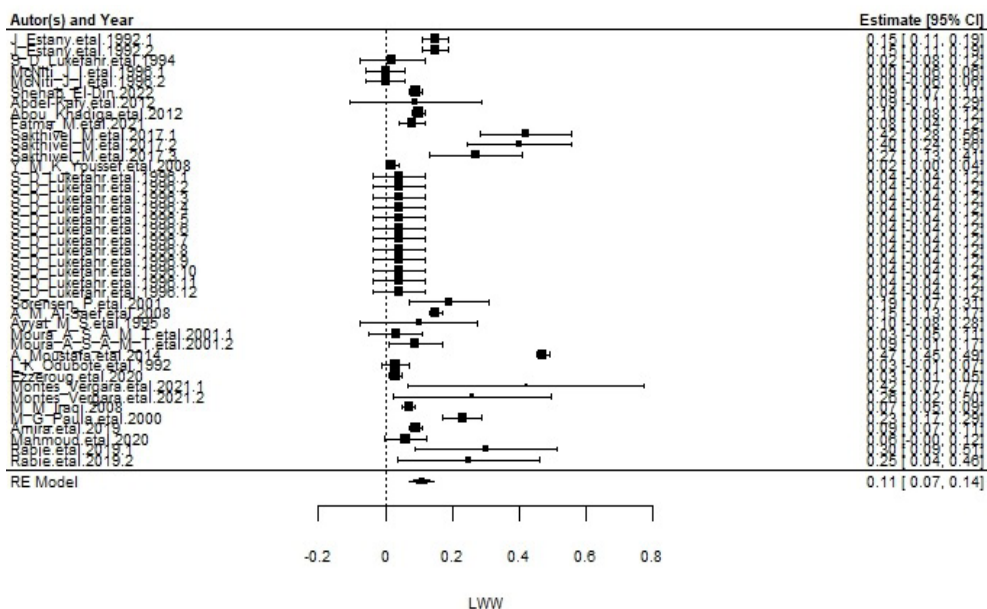
Supplementary Figure 1: The forest plot of individual studies and the overall outcome for heritability estimates of LSB in rabbit. The horizontal bars represents the 95% confidence intervals for the study.



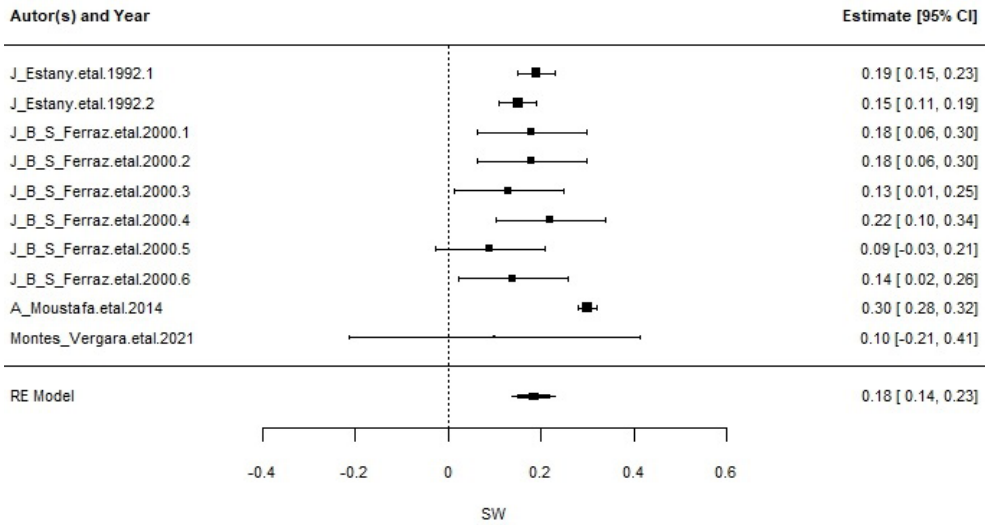
Supplementary Figure 2: The forest plot of individual studies and the overall outcome for heritability estimates of LBW in rabbit. The horizontal bars represents the 95% confidence intervals for the study.



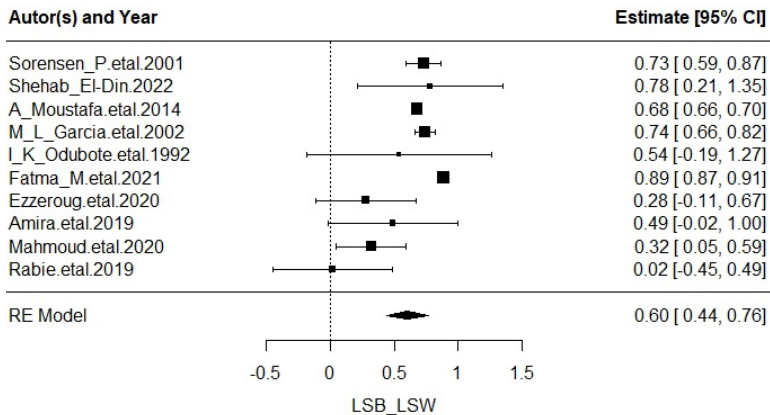
Supplementary Figure 3: The forest plot of individual studies and the overall outcome for heritability estimates of LSW in rabbit. The horizontal bars represents the 95% confidence intervals for the study.



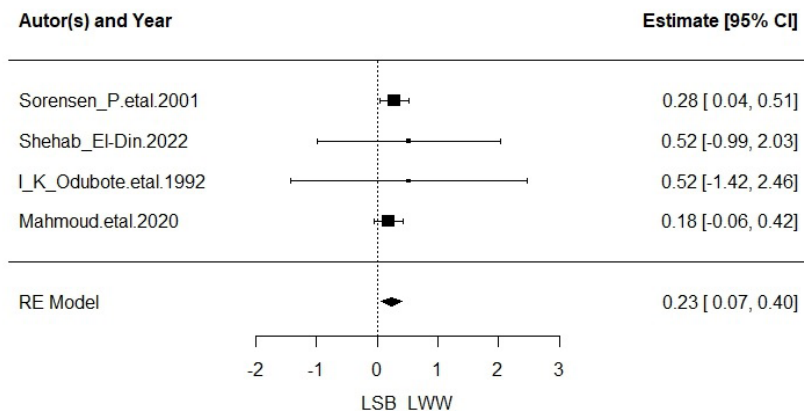
Supplementary Figure 4: The forest plot of individual studies and the overall outcome for heritability estimates of LWW in rabbit. The horizontal bars represents the 95% confidence intervals for the study.



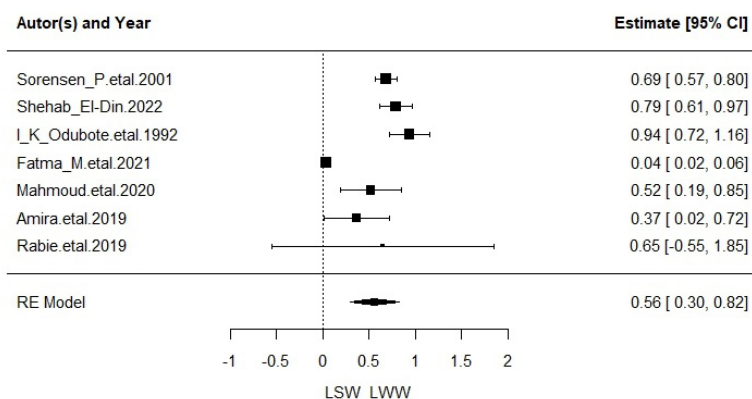
Supplementary Figure 5: The forest plot of individual studies and the overall outcome for heritability estimates of SW in rabbit. The horizontal bars represents the 95% confidence intervals for the study.



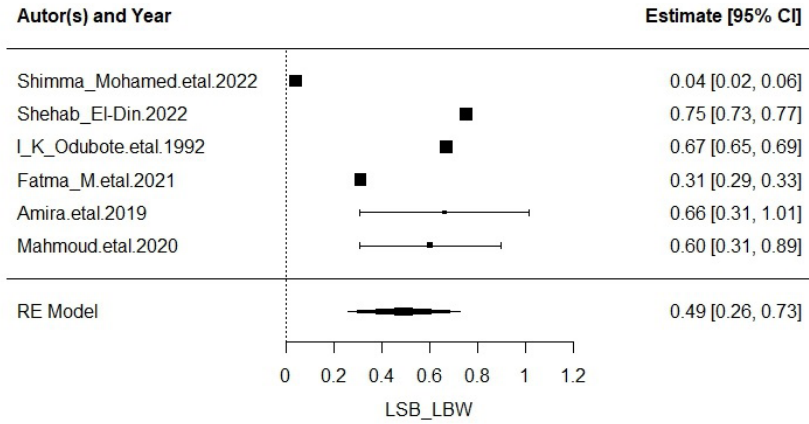
Supplementary Figure 6: The forest plot of individual studies and the overall outcome for genetic correlation estimates between LSB and LSW in rabbit. The horizontal bars represents the 95% confidence intervals for the study.



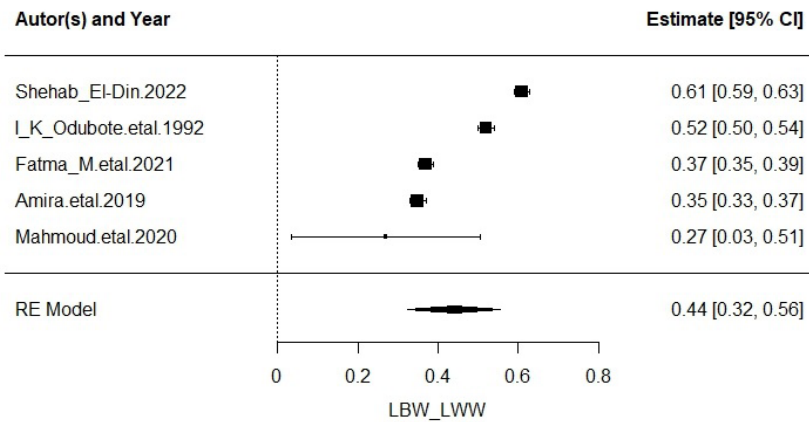
Supplementary Figure 7: The forest plot of individual studies and the overall outcome for genetic correlation estimates between LSB and LWW in rabbit. The horizontal bars represents the 95% confidence intervals for the study.



Supplementary Figure 8: The forest plot of individual studies and the overall outcome for genetic correlation estimates between LSW and LWW in rabbit. The horizontal bars represents the 95% confidence intervals for the study.



Supplementary Figure 9: The forest plot of individual studies and the overall outcome for genetic correlation estimate between LSB and LBW in rabbit. The horizontal bars represents the 95% confidence intervals for the study.



Supplementary Figure 10: The forest plot of individual studies and the overall outcome for genetic correlation estimate between LBW and LWW in rabbit. The horizontal bars represents the 95% confidence intervals for the study.

SUPPLEMENTARY FILE 1

Table S1: Details of published studies used in meta-analysis.

Number	Author (year)	Model	Method	Sample size	Breed
Litter size at birth					
1	Shehab El-Din (2022)	Animal	REML	441	Multiracial
2	Rastogi <i>et al.</i> (2000)	Animal	REML	1118	Multiracial
3	Abdel-Kafy <i>et al.</i> (2012)	Animal	REML	642	Baladi Black
4	Abou Khadiga <i>et al.</i> (2012)	Animal	REML	1400	Multiracial
5	Behiry <i>et al.</i> (2021)	Animal	REML	330	Multiracial
6	Farouk <i>et al.</i> (2022)	Animal	REML	625	New Zealand
7	Youssef <i>et al.</i> (2008)	Animal	REML	2834	Multiracial
8	Iraqi (2008)	Animal	REML	364	New Zealand
9	Sorensen <i>et al.</i> (2001)	Animal	REML	808	White Danish
10	Ragab and Baselga (2011)	Animal	REML	47 132	Multiracial
11	Al-Saef <i>et al.</i> (2008)	Animal	REML	3496	Multiracial
12	García and Baselga (2002a)	Animal	REML	12 651	Multiracial
13	Ayyat <i>et al.</i> (1995)	Animal	REML	519	New Zealand
14	Moustafa <i>et al.</i> (2014)	Animal	REML	3144	Multiracial
15	Nagy <i>et al.</i> (2014)	Animal	REML	11 582	Pannon White
16	García and Baselga (2002b)	Animal	REML	9842	Multiracial
17	Nagy <i>et al.</i> (2011)	Animal	REML	15 900	Multiracial
18	Odubote and Somade (1992)	Sire	REML	260	Multiracial
19	Ezzeroug <i>et al.</i> (2019)	Animal	REML	3242	Multiracial
20	Montes-Vergara <i>et al.</i> (2021)	Sire	REML	210	New Zealand White
21	El-Deghadi (2019)	Animal	REML	765	New Zealand White
22	El-Attrouny and Habashy (2020)	Animal	REML	3214	New Zealand White
23	Rabie <i>et al.</i> , (2019)	Animal	REML	896	Multiracial
24	Nguyen <i>et al.</i> (2017)	Animal	REML	5830	Pannon Large
25	Piles <i>et al.</i> (2006)	Animal	REML	35 776	Synthetic Lines
26	Ziadi <i>et al.</i> (2013)	Animal	BAYESIAN	3563	Synthetic Lines
Litter weight at birth					
1	Shehab El-Din (2022)	Animal	REML	441	Multiracial
2	Abdel-Kafy <i>et al.</i> (2012)	Animal	REML	642	Baladi Black
3	Abou Khadiga <i>et al.</i> (2012)	Animal	REML	1400	Multiracial
4	Behiry <i>et al.</i> (2021)	Animal	REML	330	Multiracial
5	Farouk <i>et al.</i> (2022)	Animal	REML	625	New Zealand White
6	Youssef <i>et al.</i> (2008)	Animal	REML	2833	Multiracial
7	Iraqi (2008)	Animal	REML	364	New Zealand White
8	Al-Saef <i>et al.</i> (2008)	Animal	REML	3496	Multiracial
9	Ayyat <i>et al.</i> (1995)	Animal	REML	519	New Zealand White
10	Odubote and Somade (1992)	Animal	REML	260	Multiracial
11	Montes-Vergara <i>et al.</i> (2021)	Animal	REML	210	New Zealand White
12	El-Deghadi (2019)	Animal	REML	765	New Zealand White
13	El-Attrouny and Habashy (2020)	Animal	REML	3214	New Zealand White
14	Rabie <i>et al.</i> , (2019)	Animal	REML	896	Multiracial
Litter size at weaning					
1	Sorensen <i>et al.</i> (2001)	Animal	REML	1021	White Danish
2	Shehab El-Din (2022)	Animal	REML	423	Multiracial

WEIGHTED HERITABILITY AND GENETIC CORRELATION ESTIMATE IN RABBIT

3	Rastogi <i>et al.</i> (2000)	Animal	REML	1051	Multiracial
4	Moustafa <i>et al.</i> (2014)	Animal	REML	3136	Multiracial
5	Moura <i>et al.</i> (2001)	Animal	REML	4244	Botucatu Albino
6	García and Baselga (2002a)	Animal	REML	12 651	Multiracial
7	Ragab and Baselga (2011)	Animal	REML	47 097	Multiracial
8	Iraqi (2008)	Animal	REML	364	New Zealand White
9	Odubote and Somade (1992)	Animal	REML	260	Multiracial
10	García and Baselga (2002b)	Animal	REML	9842	Multiracial
11	Behiry <i>et al.</i> (2021)	Animal	REML	330	Multiracial
12	Abou Khadiga <i>et al.</i> (2012)	Animal	REML	1400	Multiracial
13	Abdel-Kafy <i>et al.</i> (2012)	Animal	REML	322	Baladi Black
14	Al-Saef <i>et al.</i> (2008)	Animal	REML	3409	Multiracial
15	Youssef <i>et al.</i> (2008)	Animal	REML	2740	Multiracial
16	Ezzeroug <i>et al.</i> (2019)	Animal	REML	3238	Multiracial
17	El-Deghadi (2019)	Animal	REML	765	New Zealand White
18	El-Attrouny and Habashy (2020)	Animal	REML	3109	New Zealand White
19	Rabie <i>et al.</i> , (2019)	Animal	REML	896	Multiracial
20	Piles <i>et al.</i> (2006)	Animal	REML	35 776	Synthetic Lines
Litter weight at weaning					
1	Estany <i>et al.</i> (1992)	Animal	REML	17 109	Multiracial
2	Lukefahr and Atakora (1994)	Animal	REML	1453	Multiracial
3	McNitt and Lukefahr (1996)	Animal	REML	7878	New Zealand White
4	Shehab El-Din (2022)	Animal	REML	423	Multiracial
5	Abdel-Kafy <i>et al.</i> (2012)	Animal	REML	322	Baladi Black
6	Abou Khadiga <i>et al.</i> (2012)	Animal	REML	1400	Multiracial
7	Behiry <i>et al.</i> (2021)	Animal	REML	330	Multiracial
8	Sakthivel <i>et al.</i> (2017)	Animal	REML	5199	New Zealand White
9	Youssef <i>et al.</i> (2008)	Animal	REML	2740	Multiracial
10	Lukefahr <i>et al.</i> (1996)	Animal	REML	19 392	Multiracial
11	Sorensen <i>et al.</i> (2001)	Animal	REML	1014	White Danish
12	Al-Saef <i>et al.</i> (2008)	Animal	REML	3398	Multiracial
13	Ayyat <i>et al.</i> (1995)	Animal	REML	519	New Zealand White
14	Moura <i>et al.</i> (2001)	Animal	REML	4244	Botucatu Albino
15	Moustafa <i>et al.</i> (2014)	Animal	REML	10 847	Multiracial
16	Odubote and Somade (1992)	Animal	REML	260	Multiracial
17	Ezzeroug <i>et al.</i> (2019)	Animal	REML	18 472	Multiracial
18	Montes-Vergara <i>et al.</i> (2021)	Animal	REML	1490	New Zealand White
19	Cinti Iraqi (2008)	Animal	REML	364	New Zealand White
20	Paula <i>et al.</i> (2000)	Animal	REML	3249	California
21	El-Deghadi (2019)	Animal	REML	765	New Zealand White
22	El-Attrouny and Habashy (2020)	Animal	REML	3088	New Zealand White
23	Rabie <i>et al.</i> , (2019)	Animal	REML	896	Multiracial
Individual weight at slaughter					
1	Estany <i>et al.</i> (1992)	Animal	REML	17 109	Multiracial
2	Ferraz and Eler (2000)	Animal	REML	8780	Multiracial
3	Moustafa <i>et al.</i> (2014)	Animal	REML	8495	Multiracial
4	Montes-Vergara <i>et al.</i> (2021)	Animal	REML	1280	New Zealand White

META-ANALYSIS' REFERENCE

- Abdel-Kafy E.M., Hassans N.S., Morsy W.A., Ali K.A.A., El-Sawy M.A., Hassanein M.N.F., Sabra Z.A.M. 2012. Genetic parameters of litter traits in a local Baladi Black rabbit in Egypt. *In Proc.: 10th World Rabbit Congress, Septembere 3-6, 2012, Sharm El-Sheikh, Egypt*, p. 37-41.
- Abou Khadiga G., Yousef Y.M.K., Baselga M. 2012. Characterization of reproductive performance of the APRI line of rabbits. *In Proc.: 10th World Rabbit Congress, Septembere 3-6, 2012, Sharm El-Sheikh-Egypt*, p. 743-747.
- Al-Saef A.M., Khalil M.H., Al-Homidan A.H., Al-Dobaib S.N., Al-Sobayil K.A., García M.L., Baselga M. 2008. Crossbreeding effects for litter and lactation traits in a Saudi project to develop new lines of rabbits suitable for hot climates. *Livest. Sci.*, 118: 238-246. <https://doi.org/10.1016/j.livsci.2008.01.025>.
- Ayyat M.S., Marai I.F.M., El-Sayiad G.H.A. 1995. Genetic and non-genetic factors affecting milk production and preweaning litter traits of New Zealand White does under Egyptian conditions. *World Rabbit Sci.*, 3: 119-124. <https://doi.org/10.4995/wrs.1995.250>
- Behiry F.M., Gharib M.G., Elkassas N.E., Mosalm G.A. 2021. Genetic and some physiological evaluations of doe and body condition traits for the Apri rabbits. *Egypt. Poult. Sci. J.*, 41: 229-248. <https://doi.org/10.21608/EPSJ.2021.160069>
- El-Attrouny M.M., Habashy W.S. 2020. Correlated response on litter traits and milk yield in New Zealand white rabbits selected for litter size at birth. *Egypt. Poult. Sci. J.*, 40: 599-612. <https://doi.org/10.21608/EPSJ.2020.114314>
- El-Deghadi A. 2019. Factors affecting milk production and using application selection indices to improve productive traits of does in New Zealand White rabbits. *Egypt. J. Rabbit Sci.*, 29: 61-78. <https://doi.org/10.21608/ejrs.2019.45674>
- Estany J., Camacho J., Baselga M., Blasco A. 1992. Selection response of growth rate in rabbit for meat production. *Genet. Selec. Evol.*, 24: 527-537. <https://doi.org/10.1186/1297-9686-24-6-527>.
- Ezzeroug R., Belabbas R., Argente M.J., Berbar A., Diss S., Boudjella Z., Talaziza D., Boudahdir N., García M.L. 2019. Genetic correlations for reproductive and growth traits in rabbits. *Can. J. Anim. Sci.*, 100: 317-322, 2019. <https://doi.org/10.1139/cjas-2019-0049>.
- Farouk S.M., Khattab A.S., Noweir A., Hossein-Zadeh N.G. 2022. Genetic analysis of some productive and reproductive traits in New Zealand White rabbits. *World Rabbit Sci.*, 30: 141-146. <https://doi.org/10.4995/wrs.2022.15939>.
- Ferraz J.B.S., Eler J. P. 2000. Choice of animal models for estimation of genetic parameters of reproductive, growth and slaughter traits of Californian and New Zealand rabbits raised under tropical conditions. *Livest. Res. Rural Develop.*, 12: 2000.
- García M.L., Baselga M. 2002a. Estimation of genetic response to selection in litter size of rabbits using a cryopreserved control population. *Livest. Prod. Sci.*, 74: 45-53. [https://doi.org/10.1016/S0301-6226\(01\)00280-9](https://doi.org/10.1016/S0301-6226(01)00280-9).
- García M.L., Baselga M. 2002b. Genetic response to selection for reproductive performance in a maternal line of rabbits. *World Rabbit Sci.*, 10: 71-76. <https://doi.org/10.4995/wrs.2002.478>
- Iraqi M.M. 2008. Estimation of heritability and repeatability for maternal and milk production traits in New Zealand White rabbits raised in hot climate conditions, *Livest. Res. Rural Develop.*, 20: 2008.
- Lukefahr S.D., Atakora J.K.A. 1994. Genetic and environmental parameter estimation following mass selection for 70-day body weight in rabbit using an animal model. *In Proc.: World Congress on Genetics Applied to Livestock Production*. 5: 119-122.
- Lukefahr S.D., Odi H.B., Atakora J.K.A. 1996. Mass selection for 70-day body weight in rabbits. *J. Anim. Sci.*, 74: 1481-1489. <https://doi.org/10.2527/1996.7471481x>
- Mcnitt J.I., Lukefahr S.D. 1996. Genetic and environmental parameters for postweaning growth traits of rabbits using an animal model. *World Rabbit Sci. Assoc., World Rabbit Congress*, p. 325-329.
- Montes-Vergara D.E., Hernández-Herrera D.Y., Hurtado-Lugo N.A. 2021. Genetic parameters of growth traits and carcass weight of New Zealand White rabbits in a tropical dry forest area. *J. Adv. Vet. Anim. Res.*, 8: 471. <https://doi.org/10.5455/javar.2021.h536>
- Moura A.S.A.M.T., Costa A.R.C., Polastre R. 2001. Variance components and response to selection for reproductive litter and growth traits through a multi-purpose index. *World Rabbit Sci.*, 9: 77-86. <https://doi.org/10.4995/wrs.2001.449>
- Moustafa H., El-Raffa A., Shebl M.K., El-Delebsbany A., El-Sayed N. 2014. Genetic evaluation of some economic traits in a maternal line of rabbits. *Egypt. Poult. Sci. J.*, 34: 85-98. <https://doi.org/10.21608/EPSJ.2014.5308>
- Nagy I., Radnai I., Nagyné-Kiszlinger H., Farkas J., Szendrő Z. 2011. Genetic parameters and genetic trends of reproduction traits in synthetic Pannon rabbits using repeatability and multi-trait animal models. *Archiv. Anim. Breed.*, 54: 297-307. <https://doi.org/10.5194/aab-54-297-2011>
- Nagy I., Farkas J., Curik I., Gorjanc G., Gyovai P., Szendrő Z. 2014. Estimation of additive and dominance variance for litter size components in rabbits. *Czech J. Anim. Sci.*, 59: 182-189. <https://doi.org/10.17221/7342-CJAS>
- Nguyen N.T., Farkas J., Szendrő Z., Nagy I. 2017. Genetic evaluation of litter size traits in Pannon Large rabbits. *Anim. Sci. Papers and Reports*, 35: 181-192.
- Odubote, I.K., Somade, B. 1992. Genetic analysis of rabbit litter traits at birth and weaning. *Nigerian J. Anim. Prod.*, 19: 64-69. <https://doi.org/10.51791/njap.v19i.2082>
- Paula M.G., Ferraz J.B.S., Eler J.P. 2000. Parâmetros genéticos para coelhos da raça Califórnia criados no Brasil. Genetic parameters for Californian rabbits raised in Brazil. *Arquivo Brasileiro de Medicina Veterinária e Zootecnia*, 52: 544-548. <https://doi.org/10.1590/S0102-0935200000500022>.
- Piles M., García M.L., Rafel O., Ramon J., Baselga M. 2006. Genetics of litter size in three maternal lines of rabbits: Repeatability versus multiple-trait models. *J. Anim. Sci.*, 84: 2309-2315. <https://doi.org/10.2527/jas.2005-622>
- Rabie T.S.K., Nowier A.M., Abou-Zeid A.E., Khattab A.S. 2019. Impact of crossing between Gabali and V-line rabbits on the pre-weaning traits by using tri diagonal and genetic merit methods. *Egypt. Poult. Sci. J.*, 39: 519-536. <https://doi.org/10.21608/EPSJ.2019.39290>
- Ragab M., Baselga M. 2011. A comparison of reproductive traits of four maternal lines of rabbits selected for litter size at weaning and founded on different criteria. *Livest. Sci.*, 136: 201-206. <https://doi.org/10.1016/j.livsci.2010.09.009>
- Rastogi R.K., Lukefahr S.D., Lauckner F.B. 2000. Maternal heritability and repeatability for litter traits in rabbits in a humid tropical environment. *Livest. Prod. Sci.*, 67: 123-128. [https://doi.org/10.1016/S0301-6226\(00\)00180-9](https://doi.org/10.1016/S0301-6226(00)00180-9)

Sakthivel M., Balasubramanyam D., Kumarasamy P., Gopi H., Raja A., Anilkumar R., Devaki A. 2017. Estimates of (co)variance components and genetic parameters for body weights and growth efficiency traits in the New Zealand White rabbit. *World Rabbit Sci.*, 25: 329-338. <https://doi.org/10.4995/wrs.2017.7057>

Shehab El-Din M.I. 2022. Genetic analysis of pre-weaning litter traits in V-line rabbits using a single-trait animal model. *Archiv. Agric. Sci. J.*, 5: 211-225, 2022. <https://doi.org/10.21608/aasj.2022.107003.1096>

Sorensen P., Kjaer J.B., Brenoe U.T., Su G. 2001. Estimates of genetic parameters in Danish White rabbits using an animal model: II. Litter traits. *World Rabbit Sci.*, 9: 33-38. <https://doi.org/10.4995/wrs.2001.444>.

Youssef Y.M.K., Baselga M., Khalil M.H., Gad-Alla S., García M.L. 2008. Evaluation of litter traits in a crossing project of V-line and Baladi Red rabbits in Egypt. *Livest. Res. Rural Develop.*, 20.

Ziadi C., Mocé M.L., Laborda P., Blasco A., Santacreu M. A. 2013. Genetic selection for ovulation rate and litter size in rabbits: Estimation of genetic parameters and direct and correlated responses. *J. Anim. Sci.*, 91: 3113-3120, <https://doi.org/10.2527/jas.2012-6043>

SUPPLEMENTARY FILE 2

Table S2: Egger's test, number of missing studies, mean, and 95% confidence interval (95% CI) estimated through meta-analysis.

Traits	Egger's test <i>P</i> -value	Trim-and-fill method		
		Missing	Mean	95% CI
LSB - LWW	0.5621	0	0.2176	0.0870-0.4352

For traits, see Table 1. Missing: number of missing studies.

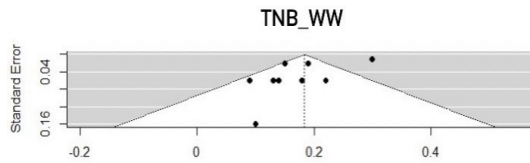


Figure S2: Funnel plot of Fisher's Z for the genetic correlation between LSB and LWW in rabbit.